

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/980,145

Source: _____

Date Processed by STIC: _____

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/19/2005

PATENT APPLICATION: US/09/980,145

TIME: 11:17:35

Input Set : N:\Crif3\RULE60\09980145.raw.txt

Output Set: N:\CRF4\01192005\I980145.raw

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1 <110> APPLICANT: Synaptic Pharmaceutical Corporation
2 <120> TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
3 <130> FILE REFERENCE: 59338-B-PCT
4 <140> CURRENT APPLICATION NUMBER: 09/980,145
5 <141> CURRENT FILING DATE: 2002-04-12
6 <150> PRIOR APPLICATION NUMBER: PCT/US00/14654
7 <151> PRIOR FILING DATE: 2000-05-26
8 <150> PRIOR APPLICATION NUMBER: 09/413,433
9 <151> PRIOR FILING DATE: 1999-10-06
10 <150> PRIOR APPLICATION NUMBER: 09/322,257
11 <151> PRIOR FILING DATE: 1999-05-28
12 <160> NUMBER OF SEQ ID NOS: 46
13 <170> SOFTWARE: PatentIn Ver. 2.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 573
17 <212> TYPE: DNA
18 <213> ORGANISM: Homo sapiens
19 <400> SEQUENCE: 1
20      actgtggact ttcttctggg gtgtctggtc atgccttaca gtatgggtgag atctgctgag 60
21      cactgttggg attttggaga agtcttctgt aaaattcaca caagcaccga cattatgctg 120
22      agctcagcct ccattttcca tttgtctttc atctccattg accgctacta tgctgtgtgt 180
23      gatccactga gatataaagc caagatgaat atcttggtta tttgtgtgat gatcttcatt 240
24      agttggagtg tccctgctgt ttttgcatth ggaatgatct ttctggagct aaacttcaaa 300
25      ggcgctgaag agatatatta caaacatggt cactgcagag gaggttgctc tgtcttcttt 360
26      agcaaaatat ctgggggtact gacctttatg acttcttttt atatacctgg atctattatg 420
27      ttatgtgtct attacagaat atatcttatc gctaaagaac aggcaagatt aattagtgat 480
28      gccaatcaga agctccaaat tggattggaa atgaaaaatg gaatttcaca aagcaaagaa 540
29      aggaaagctg tgaagacatt ggggattgtg atg                                     573
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 191
33 <212> TYPE: PRT
34 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 2
36      Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val
37      1          5          10          15
38      Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile
39      20          25          30
40      His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu
41      35          40          45
42      Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg
43      50          55          60
44      Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile
45      65          70          75          80

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46      Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu
47                85                      90                      95
48      Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys
49                100                      105                      110
50      Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr
51                115                      120                      125
52      Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr
53                130                      135                      140
54      Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp
55                145                      150                      155                      160
56      Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly Ile Ser
57                165                      170                      175
58      Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val Met
59                180                      185                      190
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 1101
63 <212> TYPE: DNA
64 <213> ORGANISM: Rattus norvegicus
65 <400> SEQUENCE: 3
66      attgctcgac agccaaaggg acagagcagc ctgtgttttag ttctctgtag tgatgcatct 60
67      ttgccacaat agcgcgaata tttcccacac gaacagcaac tgggtcaaggg atgtccgtgc 120
68      ttcgctgtac agcttaatat cactcataat tctaaccact ctgggtggca acttaatagt 180
69      aatcatttcg atatccact tcaagcaact tcacacgccc acaaattggc tccttcattc 240
70      catggccggt gtcgactttc tgctgggctg tctgggtcatg ccctacagca tgggtgagaac 300
71      agttgagcac tgctgggtact ttgggggaact cttctgcaaa cttcacacca gcactgatat 360
72      catgctgagc tcggcatcca ttctccacct agccttcatt tccattgacc gctactatgc 420
73      tgtgtgcgac cctttaagat acaaagccaa gatcaatctc gccgccattt ttgtgatgat 480
74      cctcattagc tggagccttc ctgctgtttt tgcatttggg atgatcttcc tggagctgaa 540
75      cttagaagga gttgaggagc tgtatcacaa tcaggtcttc tgccctgcgcg gctgttttcc 600
76      cttcttcagt aaagtatctg gggactggc attcatgacg tctttctata tacctggatc 660
77      tgttatgtta tttgtttact atagaatata tttcatagct aaaggacaag caaggtcaat 720
78      taatcgtgca aatcttcaag ttggattgga aggggaaagc agagcgccac aaagcaagga 780
79      aacaaaagcc gcgaaaacct tagggatcat ggtgggcgtt ttctctctgt gctgggtgcc 840
80      gttctttttc tgcattggtcc tggacccttt cctgggctat gttatcccac ccactctgaa 900
81      tgacacactg aattgggttg ggtacctgaa ctctgccttc aacccgatgg tttatgcctt 960
82      tttctatccc tggttcagaa gacggttgaa gatggttctc ttcggtaaaa ttttccaaaa 1020
83      agattcatct aggtctaagt tatttttgta acgcaatcca tgaaaccagt atattttgta 1080
84      gttcttaaga gcagttggtg a                                     1101
86 <210> SEQ ID NO: 4
87 <211> LENGTH: 332
88 <212> TYPE: PRT
89 <213> ORGANISM: Rattus norvegicus
90 <400> SEQUENCE: 4
91      Met His Leu Cys His Asn Ser Ala Asn Ile Ser His Thr Asn Ser Asn
92      1                5                10                15
93      Trp Ser Arg Asp Val Arg Ala Ser Leu Tyr Ser Leu Ile Ser Leu Ile
94      20                25                30
95      Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Ile Ser Ile Ser
96      35                40                45

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```

97   His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Leu His Ser Met
98       50                               55                               60
99   Ala Val Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met
100      65                               70                               75                               80
101   Val Arg Thr Val Glu His Cys Trp Tyr Phe Gly Glu Leu Phe Cys Lys
102                               85                               90                               95
103   Leu His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Leu His
104                               100                              105                              110
105   Leu Ala Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu
106                               115                              120                              125
107   Arg Tyr Lys Ala Lys Ile Asn Leu Ala Ala Ile Phe Val Met Ile Leu
108       130                               135                               140
109   Ile Ser Trp Ser Leu Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu
110      145                               150                               155                               160
111   Glu Leu Asn Leu Glu Gly Val Glu Glu Leu Tyr His Asn Gln Val Phe
112                               165                               170                               175
113   Cys Leu Arg Gly Cys Phe Pro Phe Phe Ser Lys Val Ser Gly Val Leu
114                               180                              185                              190
115   Ala Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Val Met Leu Phe Val
116       195                               200                               205
117   Tyr Tyr Arg Ile Tyr Phe Ile Ala Lys Gly Gln Ala Arg Ser Ile Asn
118      210                               215                               220
119   Arg Ala Asn Leu Gln Val Gly Leu Glu Gly Glu Ser Arg Ala Pro Gln
120      225                               230                               235                               240
121   Ser Lys Glu Thr Lys Ala Ala Lys Thr Leu Gly Ile Met Val Gly Val
122                               245                               250                               255
123   Phe Leu Leu Cys Trp Cys Pro Phe Phe Phe Cys Met Val Leu Asp Pro
124       260                               265                               270
125   Phe Leu Gly Tyr Val Ile Pro Pro Thr Leu Asn Asp Thr Leu Asn Trp
126       275                               280                               285
127   Phe Gly Tyr Leu Asn Ser Ala Phe Asn Pro Met Val Tyr Ala Phe Phe
128      290                               295                               300
129   Tyr Pro Trp Phe Arg Arg Ala Leu Lys Met Val Leu Phe Gly Lys Ile
130      305                               310                               315                               320
131   Phe Gln Lys Asp Ser Ser Arg Ser Lys Leu Phe Leu
132                               325                               330

```

134 <210> SEQ ID NO: 5

135 <211> LENGTH: 1038

136 <212> TYPE: DNA

137 <213> ORGANISM: Homo sapiens

138 <400> SEQUENCE: 5

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139   tcaggaatga tgcccttttg ccacaatata attaatat t cctgtgtgaa aaacaactgg 60
140   tcaa atgatg tccgtgcttc cctgtacagt ttaatggtgc tcataattct gaccacactc 120
141   gttggcaatc tgatagttat tgtttctata tcacacttca aacaacttca taccccaaca 180
142   aattggctca ttcattccat ggccactgtg gactttcttc tgggggtgtct ggtcatgcct 240
143   tacagtatgg tgagatctgc tgagcactgt tgggtattttg gagaagtctt ctgtaaaatt 300
144   cacacaagca ccgacattat gctgagctca gcctccattt tccatttgtc tttcatctcc 360
145   attgaccgct actatgctgt gtgtgatcca ctgagatata aagccaagat gaatatcttg 420
146   gttattttgtg tgatgatctt cattagttgg agtgtccctg ctgtttttgc atttgggaatg 480

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147 atctttctgg agctaaactt caaaggcgct gaagagatat attacaaaca tgttcactgc 540
148 agaggagggt gctctgtctt ctttagcaaa atatctgggg tactgacctt tatgacttct 600
149 ttttatatac ctggatctat tatgttatgt gtctattaca gaatatatct tatcgctaaa 660
150 gaacaggcaa gattaattag tgatgccaat cagaagctcc aaattggatt ggaaatgaaa 720
151 aatggaattt cacaagcaa agaaaggaaa gctgtgaaga cattggggat tgtgatggga 780
152 gttttcctaa tatgctgggtg ccctttcttt atctgtacag tcatggaccc ttttcttcac 840
153 tacattattc cacctacttt gaatgatgtg ttgatttggg ttggctactt gaactctaca 900
154 tttaatccaa tggtttatgc atttttctat ccttggttta gaaaagcact gaagatgatg 960
155 ctgtttggtg aaattttcca aaaagattca tccagggtga aattattttt ggaattgagt 1020
156 tcatagaatt attatatt 1038
158 <210> SEQ ID NO: 6
159 <211> LENGTH: 339
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 6
163 Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
164 1 5 10 15
165 Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
166 20 25 30
167 Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
168 35 40 45
169 Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
170 50 55 60
171 Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
172 65 70 75 80
173 Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
174 85 90 95
175 Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
176 100 105 110
177 His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
178 115 120 125
179 Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
180 130 135 140
181 Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
182 145 150 155 160
183 Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
184 165 170 175
185 His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
186 180 185 190
187 Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
188 195 200 205
189 Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
190 210 215 220
191 Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
192 225 230 235 240
193 Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
194 245 250 255
195 Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
196 260 265 270

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```

197      Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val
198              275                      280                      285
199      Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr
200              290                      295                      300
201      Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe
202              305                      310                      315                      320
203      Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu
204              325                      330                      335
205      Leu Ser Ser
207 <210> SEQ ID NO: 7
208 <211> LENGTH: 25
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
213 <400> SEQUENCE: 7
214      ttatgcttcc ggctcgatatg ttgtg                                     25
216 <210> SEQ ID NO: 8
217 <211> LENGTH: 26
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
222 <400> SEQUENCE: 8
223      atgtgctgca aggcgattaa gttggg                                     26
225 <210> SEQ ID NO: 9
226 <211> LENGTH: 23
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
231 <223> OTHER INFORMATION: n = A, C, T or G (or other modified base such as
232      inosine)
W--> 233 <400> 9
W--> 234      tnnkntgytg gytnccntty tty                                     23
236 <210> SEQ ID NO: 10
237 <211> LENGTH: 22
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
242 <223> OTHER INFORMATION: n = A, C, T, or G (or other modified base such as
243      inosine)
W--> 244 <400> 10
W--> 245      arnswrttnv nrtancnccnar cc                                     22
247 <210> SEQ ID NO: 11
248 <211> LENGTH: 63
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 2,3,5,14,17

Seq#:10; N Pos. 3,9,11,15,18

VARIABLE LOCATION SUMMARY

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:9; N Pos. 2,3,5,14,17

Seq#:10; N Pos. 3,9,11,15,18

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09980145.raw.txt

Output Set: N:\CRF4\01192005\I980145.raw

L:233 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:234 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9
L:234 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:245 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10
L:245 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0